*****	(TM)	*****
*************************************		建分子的一种,我们是我们的一种,我们也是我们的一种,我们的一种,我们就是我们的一种,我们就是我们的一种,我们是我们的一种,我们是我们的一种,我们们们们们们们们们们们们们们们们们们们们们们们们们们们们们们们
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protein . protein database search, using Smith-Waterman algorithm Thu Aug 6 14:06:36 1998; MasPar time 11.35 Seconds 781.822 Million cell updates/sec Run on:

Tabular output not generated.

MPsrch_pp

>US-08-813-323A-1 (324-566) from US08813323A.pep (3 of 3) 1764

Description: Perfect Score:

1 SQAEKLKELDKEIRPFRQNW.......YIKDDTIFIKVIVDTSDLPD 243 Sequence:

PAM 150 Gap 11 Scoring table:

120441 seqs, 36531193 residues Searched:

Post-processing:

Minimum Match 0% Listing first 45 summaries

pir56 1:Pir1 2:pir2 3:pir3 4:pir4 5:nrl3d Database:

Mean 45.997; Variance 110.625; scale 0.416 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Pred. No.	2 2401210	1 030-276	1 030-276	3 200-275	3.246-112	3.846-109	2.05e-98	4 486-98	1 599-49	7.396-08	3.80e-06	4 050-04	9.47P-04	•	1 98e-02	3.396-02	7.52e-02	1 27e-01	1 276-01	1 650-01		1.000.1	1 659-01	10000
	Description	CD40 recentor assessment		TNFR-associated prote	CD40-associated prote	TNF receptor associat	tumor necrosis factor	TNFR-associated prote	TNF receptor associat		in A (EC 3.4.	7	3.4	A (EC 3.4	osin -	C.	ta o		body-wall muscle trop	in, fast	(C)	ď	i E	, (•
SUMMARIES	A	149272	A55960	A55649	153498	161512	S56163	B55649	A54750	138026	A40195	S24134	HYHUMA	HYHUMB	A60364	A42908	A48040	A25561	A45488	S66520	C34787	C39816	D39816	B34787	
	DB	10	7	~	~	~	~	~	~	~	~	~		н	~	~	~	~	~	~	~	7	~	~	
	Length DB	567	568	568	543	201	501	416	409	470	260	748	746	700	283	899	704	285	284	284	245	248	248	251	
æ	당성	100.0	99.4	99.4	99.0	46.0	45.0	41.4	41.3	24.8	9.3	8.6	7.7	7.5	7.3	6.9	6.7	9.9	6.5	6.5	4.9	6.4	6.4	4.9	
	Score	1764	1754	1754	1747	811	793	730	728	437	164	151	135	132	128	121	119	116	114	114	113	113	113	113	
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hange	149272 *type complete CD40 receptor-associated factor 1 · mouse #formal_name Mus musculus #common_name house mouse 15.mar_1996 #sequence_revision 15-Mar-1996 #text_change	149272 #type complete CD40 receptor-associated factor 1 #formal_name Mus musculus #common 15-Mar-1906 #sequence_revision 15	# t y j	9272 #t 40 receptor ormal_name -Mar-1996 #	149272 CD40 r #forma 15-Mar	H	RESULT ENTRY TITLE ORGANISM
		ALIGNMENTS					
5.98e-01		205697	-	1947	6.1	108	4.5
7.70e-01	tropomyosin 3, fibrob	839816 S00084	7 (7	676	7.7.9	107	44
7.70e-01	'n	A60597	0	284	9.1	107	7 5
7.70e-01	~	A39816	N	284	6.1	107	41
7.70e-01	tropomyosin 3, fibrob	A27674	2	284	6.1	107	40
7.70e-01	alpha	107/70	4 C	# 07 07		101	9 g
7.70e-01	alpha	A25825	N I	284	9.7	107	37
7.70e-01	alpha	2TMAA	2	284	6.1	107	36
7.708-01	alpha	TMRBA	н	284	6.1	107	35
7.70e-01	tropomyosin i alpha,	AS4/8/ STMAB	4 m	284	9.1	107	30.00
7.70e-01	Ø .	A22165	C) (280		107	32
	Ä	S55467	~	243	9	107	31
3.596-01	tropomyosin - Califor	538381	4 (7	284	6.2	110	30
•	outer membrane lipopr	I40303	0	214	9.5	507	8 6
2.78e-01	acrosomal protein AZ1	563993	N	1060	6.3	111	27
	mixed-lineage protein	A53800	~	847	6.3	111	36
1.65e-01	DNA-activated protein	A57099	7	4096	6.4	113	25
1,650-01	hypothetical protein	S74703	~	535	6.4	113	24

RESULT 1 BUTTE CD40 receptor-associated factor 1 - mouse ORGANISM #formal_name Mus musculus #common_name house DATE 1960 #sequence_revision 15-Mar-1996 #t 28-Feb-1997 ACCESSIONS 149272 ACCESSIONS 149272 ACCESSIONS 149272 ACCESSIONS 149272 ALSONO G.; Cleary, A.M.; Ye, Z.S.; Hong, D.I. Baltimore, D. Balti

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SUMMARY
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                                                                                                              #authors Cheng, G.; Cleary, A.M.; Ye, Z.S.; Hong, D.I.; Lederman, S.;
Baltimore, D.
#journal Science (1995) 267:1494-1498
#title Involvement of CRAFI, a relative of TRAF, in CD40 signaling.
#cross-references WUID:95184010
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The Epstein-Barr virus transforming protein LMP1 engages signaling proteins for the tumor necrosis factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hu, H.M.; O'Rourke, K.; Boguski, M.S.; Dixit, V.M.
J. Biol. Chem. (1994) 269:30069-30072
A novel RING finger protein interacts with the cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    445 FYTGYFGYKMCARVYLNGDGMGKGTHLSLFFVIMRGEYDALLPWPFKQKVTLMLADQGSS 504
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TNRR-associated protein LAPI - human
CD40-binding protein
#formal_name Homo sapiens #common_name man
23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change
10-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                   2; Indels 0; Gaps
      A55960 *type complete
CD40 receptor-associated factor 1 - human
#formal_name Homo sapiens *common_name man
15-Mar-1996 *sequence_revision 15-Mar-1996 *text_change
                                                                                                                                                                                                                                                                                                           zinc finger
#length 568 #molecular-weight 64459 #checksum 8765
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                                                                                                                                                                                                                                            1-568 ##label RES
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#authors Sato, T.; Irie, S.; Reed, J.C.
#journal FEBS Lett. (1995) 358:113-118
#title A novel member of the TRAF family of putative signal transducing proteins binds to the cytosolic domain of CD40.
#cross-references MUID:95129692
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CD40-associated protein - human
#formal_name Homo sapiens #common_name man
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
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                                                                                                                                        *region RING finger motif
#length 568 #molecular-weight 64490 #checksum 8660
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                                          ##Iresidues 1-133,135-404,'G',406-568 ##label HUA
##cross-references GB:U15637; NID:9595910; PID:9595911
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colled coll
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                                 nucleic acid sequence not shown
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##molecule_type mRNA
1-543 ##label RES
domain of CD40.
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A novel family of putative signal transducers associated with the cytoplasmic domain of the 75 kDa tumor necrosis factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Song, H.Y.; Donner, D.B.
Blochem. J. (1995) 309:825-829
Association of a RING finger protein with the cytoplasmic
domain of the human type-2 tumour necrosis factor receptor.
S56163
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                  $56163 #type complete
tumor necrosis factor receptor-associated protein - human
INF receptor-associated protein
480 RRHLGDAFKPDPNSSSFKKPTGEMNIASGCPVFVAQTVLENGTYIKDDTIFIKVIVDTSD 539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  377 FSPAFYTSRYGYKMCLRVYLNGDGTGRGTHLSLFFVVWKGPNDALLQWPFNQKVTLMLLD 436
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10-Oct-1995 #sequence_revision 01-Dec-1995 #text_change
10-Sep-1997
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Pred. No. 3.24e-112;
51; Mismatches 35; Indels
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##cross-references GB:L35303; NID:9532620; PID:9532621
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                                                                                                                                                                                                                                                                                                                                   *cross-references MUID:94349371
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Best Local Similarity 52.7%;
Matches 98; Conservative
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##residues 1-503
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Association of a RING finger protein with the cytoplasmic
domain of the human type 2 TNF receptor.
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                                                                                                                                                                                                                                                                                    2; Gaps
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TNFR-associated protein EBI6 - human
#formal_name Homo sapiens #common_name man
23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change
10.5ep-1997
                                                                                                                                     ##molecule_type_mRNA
##residues
##cross-references EMBL:012597; NID:997527; PID:9975273
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Pred. No. 3.84e-109;
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Pred. No. 2.05e-98;
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##cross-references GB:U19261; NID:9675461; PID:9675462
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Matches 97; Conservative
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Best Local Similarity 51.3%;
Matches 100; Conservative
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#length 501
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##residues 1-42,
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A novel family of putative signal transducers associated with the cytoplasmic domain of the 75 kDa tumor necrosis factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #authors Tomasetto, C.; Regnier, C.H.; Moog-Lutz, C.; Mattel, M.G.; Chenard, M.P.; Lidereau, R.; Basset, P.; Rio, M.C. Genomics (1995) 28:367-376
#title Identification of four novel human genes amplified and overexpressed in breast carcinoma and located to the q11-q21.3 region of chromosome 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     215 SQLDREHLLSLEQRVVELQQTLAQKDQVLGKLEHSLRLMEEASFDGTFLWKITNVTKRCH 274
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                                                                                     A54750 *type complete

TNF receptor associated factor 1 - mouse
#formal_name Mus musculus #common_name house mouse
02-uil-1996 #sequence_revision 02-Jul-1996 #text_change
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I38026; S60681
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Flannery, A.V.; Macadam, G.C.; Beynon, R.J.
Biochim. Biophys. Acta (1991) 1079:119-122
Immunological characterisation of different meprin species in
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#title The alpha subunit of meprin A. Molecular cloning and sequencing, differential expression in inbred mouse strains, and evidence for divergent evolution of the alpha #cross-references MUID:92250517
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385-388;390-391, H', 393-399;402-403, F', 405-411;
414-419, I', 421-422, TVIFDRP'; GETVQGDTDVNAKAW'
##label Fine
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##molecule_type protein
##residues 34-38;78-82 ##label BEY
**cerrication #superfamily meprin A; astacin homology; EGF homology; MAM
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J.S.; Flannery, A.V.; Beynon, R.J.
#journal J. Biol. Chem. (1991) 266:21381-21385
#title The astacin family of metalloendopeptidases.
#cross-references MUID:92042028
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#formal_name Mus musculus #common_name house mouse
16-0ct-1992 #sequence_revision 16-0ct-1992 #text_change
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meprin A (EC 3.4.24.18) alpha chain precursor - mouse
Score 437; DB 2; Length 470;
Pred. No. 1.59e-49;
44; Mismatches 47; Indels 11;
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Blochem. J. (1996) 315:461-466
Characterization of the soluble, secreted form of
                                                                                                                                                                                                                                                                                                                                                                                         S17 SSSFKKP-T--GEMNIAS---GCPVFVAQTVLENGTYIKDDIFIKVIVD 560
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##residues 77-275 ##label DUM
##cross-references GB:M74897; GB:M74238
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#accession S17525
##molecule_type protein
##residues 108,'R',110,'
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Best Local Similarity 40.0%;
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                                                                                    #domain signal sequence #status experimental #label SIG\
#domain propeptide #status experimental #label PRO\
#product meprin A alpha chain #status experimental
#label MAT\
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FEBS Lett. (1992) 309-203-208
Molecular cloning of the alpha-subunit of rat endopeptidase-24.18 (endopeptidase-2) and co-localization with endopeptidase-24.11 in rat kidney by in situ
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hydrolase; metalloproteinase; transmembrane protein; zinc
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                                                                                                                                                                                                                                  #domain astacin homology #label AST\
#domain MAM homology #label MAM\
#binding_site zinc (His, His, His, Tyr) #status
Predicted\
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#length 760 #molecular-weight 85702 #checksum 4733
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#domain MAM homology #label MAM\
#binding_site zinc (His) #starus predicted\
#active_site Glu #status predicted
#active_site Glu #status predicted
#length 748 #molecular-weight 85138 #checksum 2333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 9.3%; Score 164; DB 2; Length 760; Local Similarity 30.0%; Pred. No. 7.39e-08; les 27; Conservative 25; Mismatches 34; Indels
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#cross-references MUID:92371675
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#type complete

HYHUMA

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FEBS Lett. (1993) 335:367-375
Cloning of the PABA peptide hydrolase alpha subunit
(PPH-elpha) from human small intestine and its expression
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##Cross-references GDB:371059; OMIM:600388
#map_position 6p21.2-6p21.1
MPLEX may form homodimers, homotetramers, or heterotetramers with
two alpha chains and two beta chains (see HYHUMB)
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#domain propeptide #status predicted #label PRO\
#product meprin A alpha chain #status predicted #label
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##residues 66-83 ##label DU2
##note human meprin A alpha chain appears to be expressed in
intestine but not in kidney
meprin A (EC 3.4.24.18) alpha chain precursor - human intestinal brush border metalloendopeptidase;
N-benzoyl-L-tyrosyl-p-aminobenzotc acid hydrolase; PABA peptide hydrolase (PPH) alpha chain
#formal_name Homo sapiens #common_name man 19-May-1994 #sequence_revision 16-Peb-1996 #text_change 05-Sep-1997
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J.S.; Flannery, A.V.; Beynon, R.J.
#journal J. Biol. Chem. (1991) 266:21381-21385
#title The astacin family of metalloendopeptidases.
#cross-references MUID:92042028
#accession A41196
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predicted\
14 #binding_site zinc (His, His, His, Tyr) #status
predicted\
#active_site Glu #status predicted
#length 746 #molecular-weight 84367 #checksum 7669
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##cross-references GB:M82962; GB:M74238
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##residues 1-746 ##label ELD
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Cloning of the PABA peptide hydrolase alpha subunit
(PPH-alpha) From human small intestine and its expression
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#domain propeptide #status predicted #label PRO\
#product meprin A beta chain #status predicted #label
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homology
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predicted
#length 700 #molecular-weight 79458 #checksum 916
                                                                     435 VWTVRNFSQVLENTSKGDKLQ--SPRFYNSE-GYGFGVTLYPNSRE-SSG-YLRLAFHVC 489
                                                                                                              418 IWKIRDYKRRKQEAVMGKTLSLYSQPFYTGYFGYKMCARVYLNGDGMGKGTHLSLFFVIM 477
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#domain MAW homology #label MAM\
#domain EGF homology #label EGF\
#domain Lansmembrane #status predicted #label TRW\
                                                                                                                                                                                                                                                                                             #type complete
meprin A (EC 3.4.24.18) beta chain precursor - human
N-benzoyl-L-tyrosyl-p-aminobenzoic acid hydrolase; PABA
peptide hydrolase (PPH) beta chain
#formal_name Homo sapiens #common_name man
16.Feb-1995_#sequence_revision 16.Feb-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #disulfide_bonds #status predicted\
#binding_site zinc (His, His, His, Tyr) #status
predicted\
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21; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##molecule_type protein
##residues 62-70,'S',72-73,'P',75-79 ##label DUM
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                                                                                                                                                                490 SGENDAILEWPVENRQVIITILDQEPDVRN 519
                                                                                                                                                                                           478 RGEYDALLPWPFKQK-VTLMLMDQGSSRRH 506
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       larity 28.9%;
Conservative
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    Best Local Similarity
Matches 26; Conser
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445,547,592,692
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608-619,613-628,
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608-643
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62-700
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tropomyosin - migratory locust
#formal_name Locusta migratoria #common_name migratory locust
03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change
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meprin A (EC 3.4.24.18) beta chain - rat
endopeptidase-2 beta chain; meprin beta chain; meprin-a beta
                                                                                                                                                                                                                                                                                                                                                                                                                       Krieger, J.; Raming, K.; Knipper, M.; Grau, M.; Mertens, S.;
Breer, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #superfamily meprin A; astacin homology; EGF homology; MAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence extracted from NCBI backbone (NCBIP:107784)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 EEARALOKKIOTIENDLDQTQESLGQVMAKLEEKEKALONAESEVAALNRRIQLLEEDLE 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             431 IWHIRNFIQFI-GSPNG-TL--YSPPFYSSK-GYAF--QIYLN---LAHVTNAGIYFHLI 480
                                                                                                                    418 IWKIRDYKRRKQEAVMGKTLSLYSQPFYTGYFGYKMCARVYLNGDGMGKGTHLSLFFVIM 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cloning, sequencing and expression of locust tropomyosin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24; Mismatches 34; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #formal_name Rattus norvegicus #common_name Norway rat
17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #superfamily tropomyosin
coiled coil; heptad repeat
#length 283 #molecular-weight 32439 #checksum 4917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Johnson, G.D.; Hersh, L.B.
J. Biol. Chem. (1992) 267:13505-13512
Cloning a rat meprin cDNA reveals the enzyme is
heterodimer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     heterodimer; hydrolase; metalloproteinase; zinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 283;
Score 132; DB 1; Length 700; Pred. No. 9.47e-04; 20; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             not compared with conceptual translation
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#domain MAM homology #label MAM\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 128; DB 2; I Pred. No. 2.90e-03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Insect Biochem. (1990) 20:173-184
                                                                                                                                                                 481 SGANDDQLQWPCPWQQATMTLLDQNPDIRQ 510
                                                                                                                                                                                                     478 RGEYDALLPWPFK-QKVTLMLMDQGSSRRH 506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1-283 ##label KRI
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##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.3%;
Local Similarity 21.3%;
les 16; Conservative
  Query Match
Best Local Similarity 33.3%;
Matches 30; Conservative
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A42908
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386 RHDQTLSVHDIRLAD 400
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KEYWORDS
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                                                                                                                                                                                                                                                                                            ENTRY
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#binding_site zinc (His, His, His, Tyr) #status predicted\
#active_site Glu #status predicted
#length 668 #molecular weight 75049 #checksum 9806 153,157,163,212

SUMMARY

Ouery Match 6.9%; Score 121; DB 2; Length 668; Best Local Similarity 31.6%; Pred. No. 1.98e-02; Matches 24; Conservative 19; Mismatches 26; Indels 7; Gaps 5;

495 QQATMILLDQNPDIRQ 510 | | | : |:| : |: 491 QKVILMLMDQGSSRRH 506

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Search completed: Thu Aug 6 14:07:10 1998 Job time : 34 secs.